

SEQUENCE LISTING

<110> Fischetti, Vincent
 Nelson, Daniel
 Schuch, Raymond

<120> Nucleic Acids and Polypeptides of C1
 Bacteriophage and Uses Thereof

<130> 600-1-297PCT

<150> 60/470655

<151> 2003-05-15

<160> 31

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 173

<212> PRT

<213> Bacteriophage C1 polypeptide

<400> 1

Met	Lys	Ile	Arg	Met	Lys	Thr	Ile	Tyr	Thr	Phe	Ser	Thr	Thr	Ile	Ala	
1				5					10					15		
Thr	Leu	Ala	Leu	Gly	Val	Asn	Leu	Leu	Met	Asp	Lys	Gly	Asp	Asn	Asn	
			20					25					30			
Asn	Val	Asn	Thr	Asp	Asn	Thr	Phe	Asn	Asn	Ser	Asn	Pro	Ile	Val	Gln	
		35					40					45				
Val	Asp	Asn	Asn	Ser	Ser	Glu	Ala	Thr	Thr	Thr	Ile	Thr	Ser	Asp	Thr	
	50					55					60					
Asn	Asp	Asn	Gln	Val	Ala	Ala	Asp	Asp	Thr	Asn	Asp	Thr	Glu	Gln	Leu	
65					70					75					80	
Asp	Tyr	Phe	Gln	Pro	Tyr	Glu	Tyr	Leu	Tyr	Met	Pro	Ser	Thr	Asn	Val	
				85					90					95		
Ser	Ser	Ile	Arg	Asp	Gly	Tyr	Tyr	Leu	Val	Ser	Gly	Gly	Asn	Thr	Leu	
			100					105					110			
Ala	Ala	Val	Gln	Ile	Thr	Asn	Gly	Tyr	Thr	Thr	Asp	Glu	Phe	Arg	Leu	
		115					120					125				
Lys	Asn	Ile	Ser	Ala	Glu	Gln	Trp	Thr	Val	Ser	Gln	Gln	Gln	Met	Glu	
	130					135					140					
Asp	Phe	Val	Tyr	Trp	Leu	Arg	Glu	Val	Ser	Pro	Ser	Gly	Tyr	Asn	Gln	
145					150					155					160	
Lys	Ser	Leu	Glu	Asn	Asn	Phe	Lys	Ile	Phe	Ile	Lys	Lys				
				165						170						

<210> 2

<211> 62

<212> PRT

<213> Bacteriophage C1 polypeptide

<400> 2

Met Lys Thr Gln Glu Trp Tyr Leu Val Asn Phe Gly Leu Tyr Glu Thr

1		5		10		15									
Lys	Thr	Gln	Glu	Met	Glu	Thr	Asn	Ser	Arg	Tyr	Phe	Glu	Asp	Lys	Gln
		20		25		30									
Ala	Ala	Leu	Asp	Phe	Phe	Tyr	Thr	Leu	Ala	Asn	Glu	Gly	Tyr	Tyr	Asp
		35		40		45									
Trp	Ala	His	Val	Tyr	Ser	Asn	Leu	Glu	Met	Glu	Ile	Ile	Leu		
	50			55		60									

<210> 3
 <211> 178
 <212> PRT
 <213> Bacteriophage C1 polypeptide

<400> 3
Met Lys Gln Thr Asn Ile Asp Ala Leu Phe Gly Lys Gly Asp His Gln
1 5 10 15
Leu Met Asn Lys Glu Ser Lys Tyr Leu Ser Thr Leu Phe Ile Asn Ile
20 25 30
Glu Glu Leu Ser Val His Leu Ser Ser Val Thr Leu Phe Ile Asp Glu
35 40 45
Tyr Glu Gln Leu Lys Glu Asn Ala Ile Lys Ser Lys Asn Gly Lys Cys
50 55 60
Leu Lys Leu Gly Asn Thr Leu Tyr Phe Thr Asn Asn Asn Tyr Ala Thr
65 70 75 80
Lys Leu Tyr Asn Ser Leu Leu Ala Leu Gly Phe Asn Gly Ala Asn Ser
85 90 95
Phe Ser Ser Gly Glu Gln Thr Tyr Val Ile Ser Leu Thr Gly Gly Asn
100 105 110
Ala Thr Leu Thr Thr Val Lys Thr His Tyr Gly Asp Val Lys Tyr His
115 120 125
Tyr Lys His Glu Lys Leu Pro Val Lys Lys Ile Val Asn Asp Phe Trp
130 135 140
Leu Ser Glu Gln Glu Tyr Val Tyr Thr Asn Ser Ile Lys Leu Ala Tyr
145 150 155 160
Ala Leu Leu Asp Leu Tyr Lys Thr Met Gly Tyr Ser Thr Leu Asn Thr
165 170 175
Ile Lys

<210> 4
 <211> 105
 <212> PRT
 <213> Bacteriophage C1 polypeptide

<400> 4
Met Ala Ile Asn Phe Thr Asn Ile Gly Phe Ile Asn Phe Asn Lys Glu
1 5 10 15
Tyr Asn Lys Val Leu Lys Asn Gly Ala Ile Thr Ala Ser Met Ser Ala
20 25 30
Ser Gln Lys Asp Val Lys Gly Glu Tyr Val Asp Glu Tyr His Asn Val
35 40 45
Thr Ile Pro Lys Lys Val Ala Asp Gln Ile Lys Pro Leu Ile Asn Thr
50 55 60
Glu Leu Cys Asp Ile Gln Gly Val Ile Ser Arg Asn Asp Lys Tyr Thr
65 70 75 80

Asn	Ile	Thr	Ile	Leu	Gly	Ala	Lys	Lys	His	Val	Lys	Ala	Glu	Ala	Val
				85					90					95	
Asp	Val	Ala	Asp	Glu	Asp	Leu	Pro	Phe							
			100					105							

<210> 5
 <211> 207
 <212> PRT
 <213> Bacteriophage C1 polypeptide

<400> 5															
Met	Lys	Gly	Asp	Glu	Glu	Arg	Thr	Ile	Lys	Ser	Leu	Phe	Pro	Leu	Phe
1				5					10					15	
Lys	Tyr	Met	Ala	Asn	Lys	Arg	Gln	Arg	Lys	Lys	Gln	Leu	Lys	Gln	Gln
			20				25					30			
Tyr	Gly	Val	Gly	His	Lys	Tyr	Thr	Pro	Lys	Leu	Ser	Gln	Thr	Gln	Gln
		35					40					45			
Lys	Gln	Ala	Asp	Phe	Leu	Lys	Ser	Ile	Gly	Gln	Lys	Phe	Thr	Asn	Tyr
	50					55					60				
Gln	Thr	Val	Thr	Ile	Asp	Lys	Thr	Tyr	Ser	Lys	Asn	Gln	Glu	Leu	Leu
65				70						75				80	
Asp	Thr	Ala	Asn	Glu	Ala	Leu	His	Arg	Leu	Gly	Ile	Phe	Phe	Asp	Gly
			85						90					95	
Ser	Glu	Lys	Ile	Lys	Leu	Gln	Gln	Val	Thr	Asp	Asp	Asp	Leu	Arg	Tyr
			100					105					110		
Ile	Ile	Asn	Lys	Leu	Gln	Pro	Leu	Leu	Glu	Ser	Val	Thr	Met	Arg	Tyr
		115				120						125			
Lys	Lys	Phe	Leu	Thr	Asn	Thr	Tyr	Arg	Ser	Asn	Asn	Arg	Asp	Tyr	Arg
	130					135					140				
Leu	Asp	Trp	Leu	Leu	Lys	Ser	Ala	Ile	Ser	Lys	Lys	Leu	Lys	Asn	Ala
145					150					155				160	
Gln	Thr	Val	Arg	Gly	Leu	Val	Val	Ala	Ile	Asn	Lys	Met	Asp	Arg	Asp
			165						170					175	
Phe	Lys	Glu	Tyr	Asp	Lys	Lys	Leu	Arg	Lys	Ser	Ser	Lys	Gln	Gly	Asn
			180					185					190		
Pro	Phe	Gly	Phe	Val	Val	Val	Lys	Tyr	Ser	Glu	Met	Gly	Leu	Met	
		195					200					205			

<210> 6
 <211> 408
 <212> PRT
 <213> Bacteriophage C1 polypeptide

<400> 6															
Met	Ala	Arg	Lys	Val	Lys	Lys	Thr	Ile	Lys	Thr	Ile	Phe	Lys	Asn	Glu
1				5					10					15	
Glu	Glu	Glu	Phe	Lys	Thr	Leu	Leu	Asn	Asp	Tyr	Arg	Lys	Lys	Tyr	Leu
			20					25					30		
Pro	Ser	Lys	Tyr	Asn	Gln	Leu	Glu	Leu	Leu	Asp	Trp	Leu	Cys	Ser	Asp
		35					40					45			
Glu	Ile	Leu	His	Tyr	Met	Ser	Ile	Thr	Ser	Arg	Gly	Asp	Gly	Lys	Ser
	50					55					60				
Phe	Asn	Tyr	Ile	Gly	Ala	Leu	Ala	Trp	Leu	Ser	Tyr	His	Leu	Asn	Phe
65				70						75				80	
Gly	Thr	Met	Leu	Leu	Val	Arg	His	Trp	Ser	Leu	Met	Asp	Lys	Met	Ala

Val	Phe	Asn	His	Phe	Lys	Gln	Leu	Phe	Asp	Phe	Ile	Glu	Lys	Ser	Lys	65	70	75	80
Ile	Arg	Lys	Ser	Ile	Glu	Phe	Arg	Leu	Ile	Phe	His	Asn	Gly	Ala	Lys	85	90	95	
Tyr	Asp	Asn	His	Phe	Met	Val	Ser	Glu	Ile	Gln	Arg	Asp	Ile	Asp	Asn	100	105	110	
Val	Arg	Leu	Phe	Asn	Gln	Thr	Ile	Lys	Gln	Val	Asn	His	Ile	Thr	Asp	115	120	125	
Leu	Asp	Leu	Ser	Lys	Lys	Gln	Gly	Lys	Gln	Met	Arg	Asn	Asp	Val	Asn	130	135	140	
Met	Val	Leu	Glu	Arg	Arg	Val	Arg	Ser	Ser	Asn	Asn	Leu	Asp	Gly	Asp	145	150	155	160
Met	Trp	Ile	Tyr	Gly	Arg	His	Tyr	Glu	Met	Val	Asp	Ser	Tyr	Arg	Lys	165	170	175	
Thr	Asn	Val	Ser	Ile	Glu	Leu	Cys	Gly	Arg	Met	Leu	Leu	Asn	Asn	Gly	180	185	190	
Leu	Ile	Asp	Glu	Gln	Tyr	Leu	Lys	Thr	Asp	Phe	Glu	Tyr	Asp	Lys	Tyr	195	200	205	
Asp	Leu	Asp	Thr	Asp	Leu	Thr	Trp	His	Glu	Val	Arg	Lys	Tyr	Arg	Glu	210	215	220	
Phe	Ile	Phe	Asn	Asp	Leu	Asp	Glu	Lys	Gln	Met	Lys	Tyr	Ile	His	Asn	225	230	235	240
Asp	Val	Ile	Ile	Leu	Ala	Leu	Thr	Cys	Lys	His	Tyr	Ser	Lys	Leu	Phe	245	250	255	
Tyr	Gly	Phe	Asp	Phe	Glu	Lys	Gln	Thr	Phe	Thr	Gln	Asn	Ile	Lys	Glu	260	265	270	
Glu	Tyr	Ala	Asn	Tyr	Asn	Asp	Met	Ala	Lys	Phe	Gln	Leu	Leu	Lys	Gln	275	280	285	
Ile	Gly	Asp	Asn	Met	Thr	Gly	Lys	His	Leu	Lys	Leu	Thr	Asp	Tyr	Phe	290	295	300	
Ile	Gln	Gly	Gln	Asn	Ala	Tyr	Asp	Tyr	Phe	Lys	Asn	Tyr	Tyr	Asn	Gly	305	310	315	320
Gly	Leu	Asn	Leu	Tyr	Asn	Asp	Lys	Tyr	Ile	Gly	Lys	Lys	Leu	Val	Arg	325	330	335	
Asp	Gly	Phe	Ser	Ile	Asp	Leu	Asn	Ser	Ser	Tyr	Pro	Thr	Val	Met	Tyr	340	345	350	
Lys	Glu	Lys	Leu	Pro	Thr	Phe	Leu	Val	Met	Val	Asp	Ser	Lys	Pro	Thr	355	360	365	
Asp	Leu	Lys	Asn	Ile	Gly	Ser	Thr	Asp	Gly	Asp	Tyr	Met	Val	Phe	Phe	370	375	380	
Asn	Met	Leu	Met	Glu	Asp	Val	Asn	Asp	Gln	Ile	Leu	Ser	Arg	Ile	Lys	385	390	395	400
Ser	Asn	Val	Ile	Lys	Ser	Ala	Ile	Val	Lys	Tyr	Trp	Arg	Val	Lys	Asp	405	410	415	
Gly	Tyr	Val	Trp	Leu	Asn	Asn	Val	Met	Ile	Ser	Leu	Ile	Glu	Glu	Ile	420	425	430	
Thr	His	Gln	Lys	Phe	Asn	Asn	Leu	His	Val	Gln	Ser	Phe	Ser	Val	Phe	435	440	445	
Glu	Cys	His	His	Phe	Gly	Ala	Arg	Asp	Ile	Ile	Ala	Lys	Asn	Tyr	Phe	450	455	460	
Ile	Lys	Thr	Gln	Gly	Lys	Met	Ser	Lys	Ala	Leu	Asn	Cys	Thr	Met	Glu	465	470	475	480
Thr	Ile	Asp	Pro	Leu	Asn	Ile	Glu	Leu	Thr	Asp	Lys	Asp	Lys	Pro	Lys	485	490	495	
Glu	Tyr	Asp	Phe	Ser	His	Glu	Met	Val	Glu	Gly	Ser	Lys	Val	Leu	Leu	500	505	510	
Asn	Gly	Ile	Tyr	Gly	Ile	Pro	Ala	Leu	Arg	Ala	Tyr	Phe	Asp	Cys	Tyr				

<210> 9
 <211> 72
 <212> PRT
 <213> Bacteriophage C1 light chain of PlyC (PlyC B)
 (formerly known as the alpha subunit)

<400> 9
 Met Ser Lys Ile Asn Val Asn Val Glu Asn Val Ser Gly Val Gln Gly
 1 5 10 15
 Phe Leu Phe His Thr Asp Gly Lys Glu Ser Tyr Gly Tyr Arg Ala Phe
 20 25 30
 Ile Asn Gly Val Glu Ile Gly Ile Lys Asp Ile Glu Thr Val Gln Gly
 35 40 45
 Phe Gln Gln Ile Ile Pro Ser Ile Asn Ile Ser Lys Ser Asp Val Glu
 50 55 60
 Ala Ile Arg Lys Ala Met Lys Lys
 65 70

<210> 10
 <211> 105
 <212> PRT
 <213> Bacteriophage C1 polypeptide

<400> 10
 Met Ile Glu Glu Trp Val Lys His Pro Ser Leu Asn Tyr Tyr Ile Ser
 1 5 10 15
 Ser Tyr Gly Arg Val Lys Asn Ser Lys Gly Leu Ile Met Lys Gln His
 20 25 30
 Ile Cys Asn Gly Tyr Lys Arg Ile Lys Leu Val Lys Asp Gly Ile Lys
 35 40 45
 Lys Asn Tyr Tyr Val His Arg Leu Val Ala Glu Thr Phe Ile Pro Lys
 50 55 60
 Leu His Val Asp Tyr Val Val His His Ile Asp His Asp Lys Leu Asn
 65 70 75 80
 Asn Trp Val His Asn Leu Glu Trp Cys His Tyr Gln Thr Asn Leu Leu
 85 90 95
 Tyr Glu Arg Glu Asn Leu Phe Asn Glu
 100 105

<210> 11
 <211> 472
 <212> PRT
 <213> Bacteriophage C1 heavy chain of PlyC (PlyC A)
 (formerly known as the beta subunit)

<400> 11
 Met Lys Gly Arg Ile Tyr Leu Met Ser Lys Lys Tyr Thr Gln Gln Gln
 1 5 10 15
 Tyr Glu Lys Tyr Leu Ala Gln Pro Ala Asn Asn Thr Phe Gly Leu Ser
 20 25 30
 Pro Gln Gln Val Ala Asp Trp Phe Met Gly Gln Ala Gly Ala Arg Pro
 35 40 45
 Val Ile Asn Ser Tyr Gly Val Asn Ala Ser Asn Leu Val Ser Thr Tyr
 50 55 60
 Ile Pro Lys Met Gln Glu Tyr Gly Val Ser Tyr Thr Leu Phe Leu Met

65					70					75					80
Tyr	Thr	Val	Phe	Glu	Gly	Gly	Gly	Ala	Gly	Asn	Trp	Ile	Asn	His	Tyr
			85						90					95	
Met	Tyr	Asp	Thr	Gly	Ser	Asn	Gly	Leu	Glu	Cys	Leu	Glu	His	Asp	Leu
			100					105					110		
Gln	Tyr	Ile	His	Gly	Val	Trp	Glu	Thr	Tyr	Phe	Pro	Pro	Ala	Leu	Ser
		115					120					125			
Ala	Pro	Glu	Cys	Tyr	Pro	Ala	Thr	Glu	Asp	Asn	Ala	Gly	Ala	Leu	Asp
	130					135					140				
Arg	Phe	Tyr	Gln	Ser	Leu	Pro	Gly	Arg	Thr	Trp	Gly	Asp	Val	Met	Ile
145					150					155					160
Pro	Ser	Thr	Met	Ala	Gly	Asn	Ala	Trp	Val	Trp	Ala	Tyr	Asn	Tyr	Cys
			165						170					175	
Val	Asn	Asn	Gln	Gly	Ala	Ala	Pro	Leu	Val	Tyr	Phe	Gly	Asn	Pro	Tyr
			180					185					190		
Asp	Ser	Gln	Ile	Asp	Ser	Leu	Leu	Ala	Met	Gly	Ala	Asp	Pro	Phe	Thr
		195					200					205			
Gly	Gly	Ser	Ile	Thr	Gly	Asp	Gly	Lys	Asn	Pro	Ser	Val	Gly	Thr	Gly
	210					215						220			
Asn	Ala	Thr	Val	Ser	Ala	Ser	Ser	Glu	Ala	Asn	Arg	Glu	Lys	Leu	Lys
225					230					235					240
Lys	Ala	Leu	Thr	Asp	Leu	Phe	Asn	Asn	Asn	Leu	Glu	His	Leu	Ser	Gly
			245					250						255	
Glu	Phe	Tyr	Gly	Asn	Gln	Val	Leu	Asn	Ala	Met	Lys	Tyr	Gly	Thr	Ile
			260					265					270		
Leu	Lys	Cys	Asp	Leu	Thr	Asp	Asp	Gly	Leu	Asn	Ala	Ile	Leu	Gln	Leu
		275					280					285			
Ile	Ala	Asp	Val	Asn	Leu	Gln	Thr	Asn	Pro	Asn	Pro	Asp	Lys	Pro	Thr
	290					295					300				
Val	Gln	Ser	Pro	Gly	Gln	Asn	Asp	Leu	Gly	Ser	Gly	Ser	Asp	Arg	Val
305					310					315					320
Ala	Ala	Asn	Leu	Ala	Asn	Ala	Gln	Ala	Gln	Val	Gly	Lys	Tyr	Ile	Gly
			325						330					335	
Asp	Gly	Gln	Cys	Tyr	Ala	Trp	Val	Gly	Trp	Trp	Ser	Ala	Arg	Val	Cys
			340					345					350		
Gly	Tyr	Ser	Ile	Ser	Tyr	Ser	Thr	Gly	Asp	Pro	Met	Leu	Pro	Leu	Ile
		355					360					365			
Gly	Asp	Gly	Met	Asn	Ala	His	Ser	Ile	His	Leu	Gly	Trp	Asp	Trp	Ser
	370					375					380				
Ile	Ala	Asn	Thr	Gly	Ile	Val	Asn	Tyr	Pro	Val	Gly	Thr	Val	Gly	Arg
385					390					395					400
Lys	Glu	Asp	Leu	Arg	Val	Gly	Ala	Ile	Trp	Cys	Ala	Thr	Ala	Phe	Ser
			405						410					415	
Gly	Ala	Pro	Phe	Tyr	Thr	Gly	Gln	Tyr	Gly	His	Thr	Gly	Ile	Ile	Glu
			420					425					430		
Ser	Trp	Ser	Asp	Thr	Thr	Val	Thr	Val	Leu	Glu	Gln	Asn	Ile	Leu	Gly
		435					440					445			
Ser	Pro	Val	Ile	Arg	Ser	Thr	Tyr	Asp	Leu	Asn	Thr	Phe	Leu	Ser	Thr
	450					455					460				
Leu	Thr	Gly	Leu	Ile	Thr	Phe	Lys								
465					470										

<210> 12

<211> 574

<212> PRT

<213> Bacteriophage C1 polypeptide

<400> 12

Met	Thr	Leu	Ser	Lys	Ile	Lys	Leu	Phe	Tyr	Asn	Thr	Pro	Phe	Asn	Asn	
1				5					10					15		
Met	Gln	Asn	Thr	Leu	His	Phe	Asn	Ser	Asn	Glu	Glu	Arg	Asp	Ala	Tyr	
			20				25						30			
Phe	Asn	Ser	Lys	Phe	Asp	Val	His	Glu	Phe	Thr	Ser	Thr	Phe	Asn	Tyr	
	35					40					45					
Arg	Asn	Met	Lys	Gly	Val	Leu	Arg	Val	Thr	Ile	Asp	Leu	Val	Ser	Asp	
50						55					60					
Arg	Ser	Cys	Phe	Glu	Gln	Leu	Met	Gly	Val	Asn	Tyr	Cys	Gln	Val	Gln	
65				70						75					80	
Tyr	Ile	Gln	Ser	Asn	Arg	Val	Glu	Tyr	Leu	Phe	Val	Thr	Asp	Ile	Gln	
				85					90					95		
Gln	Leu	Asn	Asp	Lys	Val	Cys	Glu	Leu	Ser	Leu	Val	Pro	Asp	Val	Val	
			100					105					110			
Met	Thr	Tyr	Thr	Gln	Gly	Asn	Val	Leu	Asn	Thr	Leu	Asn	Asn	Val	Asn	
		115					120						125			
Val	Ile	Arg	Gln	His	Tyr	Thr	Gln	Thr	Glu	Tyr	Glu	Gln	Asn	Leu	Glu	
	130					135					140					
Gln	Ile	Arg	Ser	Asn	Asn	Asp	Val	Leu	Ala	Thr	Ser	Thr	Met	Arg	Val	
145					150					155					160	
His	Ala	Ile	Lys	Ser	Glu	Leu	Phe	Thr	Gln	Leu	Glu	Tyr	Ile	Leu	Thr	
				165					170					175		
Ile	Gly	Ala	Asn	Leu	Arg	Lys	Ser	Phe	Gly	Thr	Ala	Glu	Lys	Pro	Lys	
			180					185					190			
Phe	Pro	Ser	Ser	Ser	Gly	Ser	Thr	His	Asp	Gly	Ile	Tyr	Asn	Pro	Tyr	
		195					200					205				
Asp	Met	Tyr	Trp	Phe	Asn	Asp	Tyr	Glu	Ser	Leu	Lys	Glu	Val	Met	Asp	
210						215					220					
Tyr	Leu	Thr	Gly	Tyr	Pro	Trp	Ile	Gln	Gln	Ser	Ile	Lys	Asn	Val	Thr	
225					230					235					240	
Ile	Ile	Pro	Ser	Gly	Phe	Ile	Lys	Gln	Glu	Ser	Leu	Asn	Asp	His	Glu	
				245					250					255		
Pro	Val	Asn	Gly	Gly	Asp	Leu	Ser	Val	Arg	Lys	Leu	Gly	Lys	Gln	Gly	
			260					265					270			
Val	Ser	Asn	Gln	Lys	Asp	Phe	Asn	Ala	Ile	Ser	Leu	Asp	Tyr	Gln	Ser	
		275					280					285				
Leu	Met	Phe	Thr	Leu	Gly	Leu	Asn	Pro	Ile	Asn	Asp	Lys	His	Leu	Leu	
290						295					300					
Arg	Pro	Asn	Ile	Val	Thr	Ala	Glu	Leu	Thr	Asp	Tyr	Ala	Gly	Asn	Arg	
305					310					315					320	
Leu	Pro	Ile	Asp	Leu	Ser	Leu	Ile	Glu	Thr	Asn	Leu	Glu	Phe	Asp	Ser	
				325					330					335		
Phe	Val	Thr	Met	Gly	Ala	Lys	Asn	Glu	Ile	Lys	Val	Tyr	Val	Lys	Asn	
			340					345					350			
Tyr	Asn	Ala	Arg	Gly	Asn	Asn	Val	Gly	Gln	Tyr	Ile	Asp	Asn	Ala	Leu	
	355						360					365				
Thr	Ile	Asn	Asn	Phe	Asp	Thr	Ile	Gly	Phe	Ser	Val	Asp	Ser	Gly	Glu	
	370					375					380					
Leu	Gly	Lys	Ala	Asn	Ser	Ala	Tyr	Ser	Arg	Glu	Leu	Ser	Asn	Ser	Arg	
385					390					395					400	
Gln	Met	Ser	Ser	Arg	Ile	Asn	Thr	Val	Leu	Asp	Asn	Asp	Ala	Ser	Val	
				405					410					415		
Lys	Asp	Arg	Leu	Phe	Asn	Ala	Ile	Ser	Leu	Ser	Gly	Gly	Leu	Ser	Ile	
			420					425					430			
Lys	Ser	Ala	Leu	Ser	Gly	Phe	Asn	Asn	Glu	Tyr	Glu	His	Tyr	Arg	Asp	

Asp	Pro	Asn	Gly	Gly	Met	Asn	Leu	Leu	Tyr	Gln	Ser	His	Thr	Phe	Gln
			260					265					270		
Val	Arg	Gly	Val	Thr	Lys	Arg	Phe	Glu	Phe	Leu	Leu	Leu	Asp	Ile	Trp
		275					280					285			
His	Met	Thr	Phe	Arg	Gly	Thr	Gly	Trp	Pro	Glu	Gln	Val	Ala	Asp	Met
	290					295					300				
Tyr	Tyr	Phe	Met	Leu	Asp	Ile	Tyr	Ala	Glu	Gly	Val	Thr	Asp	Arg	Leu
305					310					315					320
Lys	His	Val	Leu	Ser	Asn	Asn	Ala	Ile	Thr	Met	Asn	Asp	Phe	His	Gln
				325					330					335	
Phe	Asp	Asn	Asn	Ala	Gln	Val	Lys	Lys	Trp	Tyr	Pro	Val	Val	Phe	Thr
		340						345					350		
Leu	Tyr	Gly	Asn	Asp	Asp	Lys	Glu	Met	Tyr	Leu	Val	Ala	Gln	Gly	
		355					360					365			
Leu	Gly	Thr	Ser	Gly	Leu	Asp	Thr	Glu	Ser	Leu	Asp	Asn	Phe	Arg	Ala
	370					375					380				
Pro	Ala	Thr	Gly	Thr	Pro	Tyr	Val	Ile	Glu	Thr	Trp	Leu	Asp	Pro	Val
385					390					395					400
Thr	Gly	Thr	Glu	Tyr	Met	Pro	Ala	Tyr	Gln	Ala	Asp	Gly	Tyr	Lys	His
				405					410					415	
Lys	Pro	Phe	Asn	Gln	Trp	Val	Thr	Val	Glu	Asp	Phe	Tyr	Ser		
			420					425					430		

<210> 14

<211> 236

<212> PRT

<213> Bacteriophage C1 polypeptide

<400> 14

Met	Arg	Leu	Phe	Glu	Leu	Ile	Tyr	Lys	Glu	Val	Val	Lys	Asn	Gly	Tyr
1				5					10					15	
Ser	Pro	Phe	Arg	Ser	Pro	Glu	Asn	Arg	Ile	Val	Val	Phe	Glu	Asp	Lys
			20					25					30		
Ala	Gln	Ile	Glu	Thr	Lys	Ile	Met	Met	Tyr	Asp	Glu	Asp	Val	Gln	Lys
		35					40					45			
Val	Val	Asn	Glu	Leu	Ile	Phe	Thr	Gly	Ser	Lys	Val	Asn	Glu	Asp	Phe
	50					55					60				
Arg	Glu	Glu	Phe	Val	Asn	Tyr	Phe	Phe	Asn	Arg	Glu	Pro	His	Trp	Asp
65					70				75						80
Ser	Leu	Tyr	Ile	Phe	Arg	Ala	Lys	Leu	Lys	Gly	Ile	Leu	Lys	Thr	Lys
				85					90					95	
Glu	Ala	Val	Leu	Asn	Met	Leu	Tyr	Leu	Lys	Ser	Thr	Glu	Leu	Leu	Leu
			100					105					110		
Gly	Glu	Ser	Met	Ser	Lys	Ser	Glu	Gly	His	Ser	Ser	Asn	Glu	Asn	Arg
		115					120					125			
Ser	Arg	Asp	Asn	Ser	Thr	Asn	Glu	Ser	Asn	Gly	Glu	Asn	Arg	Gly	Ala
	130					135					140				
Asn	Ala	His	Ser	Thr	Asn	Pro	Asp	Asp	Val	Thr	Asp	Thr	Asp	Leu	Glu
145					150					155					160
Thr	Ala	Asn	Leu	Ser	Tyr	Ala	Asp	Asn	Leu	Asp	Lys	Ser	Tyr	Asn	Glu
				165					170					175	
Ser	Val	Asn	Val	Ser	His	Ser	Lys	Gly	Ile	Ser	Ser	Ser	Gln	Gly	Ser
			180					185					190		
Ser	Asn	Asn	Asn	Ser	Asn	Ser	Thr	Asn	Thr	Gln	Phe	Asn	Thr	Lys	Ala
		195					200					205			
Leu	Glu	Glu	Tyr	Glu	Ala	Phe	Lys	Gln	Lys	Ile	Phe	Asp	Glu	Leu	Asp

210		215		220
Ile Lys Leu Phe Ser	Gln Leu Phe Tyr Glu	Gly Tyr		
225	230	235		

<210> 15
 <211> 317
 <212> PRT
 <213> Bacteriophage C1 polypeptide

<400> 15

Met	Gln	Ile	Thr	Ser	Gly	Ile	Lys	Pro	Ser	Glu	Met	Asn	Tyr	Lys	Met
1				5					10					15	
Ser	Thr	Phe	Thr	Asp	Asp	Ile	Ala	Glu	Arg	Val	Lys	Leu	His	Lys	Gln
			20					25					30		
Asn	Tyr	Phe	Asn	Ile	Ile	Tyr	Ser	Arg	Tyr	Val	Glu	Phe	Leu	Pro	Leu
		35					40					45			
Leu	Ile	Ser	Tyr	Glu	Asn	Tyr	Asp	Leu	Asp	Ser	Leu	Leu	Ile	Glu	Ser
	50					55					60				
Tyr	Leu	Arg	Ala	Gly	Tyr	Gly	Val	Ala	Ile	Gly	Glu	Thr	Lys	Thr	Gly
65					70					75					80
Lys	Ile	Asp	Val	Leu	Gly	Tyr	Cys	Ser	Val	Asn	Thr	Asn	Tyr	Leu	Gln
				85					90					95	
Pro	Ile	Lys	Glu	Pro	Leu	Gln	Gly	Lys	Asp	Ile	Thr	Phe	Ile	His	Asn
			100					105					110		
Asn	Ile	Leu	Pro	Lys	Gly	Lys	Tyr	Lys	Glu	Leu	Thr	Arg	Tyr	Ser	Asp
		115					120					125			
Gly	Asn	Phe	Val	Val	Leu	Arg	Asn	Lys	Arg	Ala	Ser	Phe	Leu	Cys	Asp
	130					135					140				
Tyr	Asn	Ile	Ile	Thr	His	Tyr	Val	Met	Glu	Met	Ser	Glu	Ile	Ala	Asn
145					150					155					160
Ser	Arg	Tyr	Ser	Ile	Ser	Ile	Gln	Ala	Lys	Val	Asn	Thr	Phe	Ile	Arg
				165					170					175	
Asn	Glu	Gly	Gly	Ser	Lys	Asp	Gly	Gln	Val	Met	Ala	Asn	Asn	Leu	Phe
			180					185					190		
Asn	Gly	Val	Pro	Tyr	Thr	Ala	Thr	Thr	Pro	Lys	Phe	Asp	Pro	Glu	Glu
		195					200					205			
His	Ile	Leu	Thr	Phe	Asn	Asn	Ala	Ser	Ala	Val	Ser	Phe	Leu	Pro	Glu
	210					215					220				
Leu	Lys	Arg	Glu	Gln	Gln	Asn	Lys	Ile	Ser	Glu	Leu	Asn	Ala	Met	Leu
225					230					235					240
Gly	Leu	Asn	Thr	Leu	Gly	Val	Asp	Lys	Glu	Ser	Gly	Val	Ser	Glu	Ile
				245					250					255	
Glu	Ala	Gln	Ser	Asn	Thr	Ala	Phe	Lys	Lys	Ala	Asn	Glu	Asn	Ile	Tyr
			260					265					270		
Leu	Gly	Ile	Arg	Asn	Glu	Ala	Leu	Asn	Leu	Ile	Asn	Asn	Lys	Tyr	Gly
		275					280					285			
Leu	Asn	Ile	His	Ala	Glu	Tyr	Arg	Asp	Asn	Met	Val	Ala	Glu	Leu	Ser
	290					295					300				
Ser	Ile	Glu	Lys	Leu	Gln	Ile	Val	Ser	Glu	Val	Ala	Gln			
305					310					315					

<210> 16
 <211> 392
 <212> PRT
 <213> Bacteriophage C1 polypeptide

<400> 16

Met	Ala	Asp	Glu	Thr	Thr	Asn	Val	Ala	Gly	Ala	Ile	Val	Ala	Ser	Leu
1				5					10					15	
Asn	Asp	Phe	Asn	Ala	Asp	Asn	Gly	Lys	Ser	Trp	Thr	Phe	Gly	Thr	Asn
			20					25					30		
Trp	Asn	Ala	Val	Gly	Thr	Asp	Phe	Glu	Thr	Tyr	Thr	Asn	Gln	Tyr	Leu
		35					40					45			
Phe	Pro	Lys	Leu	Asn	Glu	Thr	Leu	Ile	Val	Glu	Thr	Ala	Ala	Gly	Asn
	50				55					60					
Arg	Leu	Asp	Trp	Leu	Ala	Lys	Glu	Ile	Asp	Phe	Ile	Gly	Gln	Tyr	Ser
65					70				75					80	
Glu	Glu	Tyr	Val	Ile	Leu	Asp	Thr	Val	Pro	Val	Glu	Leu	Asp	Leu	Ser
			85					90					95		
Lys	Ser	Ala	Gln	Leu	Met	Leu	Glu	Arg	Asn	Tyr	Pro	Lys	Ile	Ala	Ser
			100					105					110		
Lys	Leu	Tyr	Gly	Ala	Gly	Ile	Leu	Lys	Lys	Leu	Lys	Phe	Thr	Leu	Asn
		115					120					125			
Asp	Asn	Ile	Gln	Arg	Gln	Gln	Phe	Ala	Thr	Leu	Gly	Asp	Ala	Thr	Lys
	130					135					140				
Phe	Ala	Val	Gln	Val	Tyr	Lys	Lys	Lys	Ile	Ala	Asp	Ile	Asn	Ile	Ser
145					150					155				160	
Glu	Glu	Gln	Glu	Leu	Lys	Ala	Ile	Ile	Met	Asp	Tyr	Thr	Ser	His	Ile
			165					170						175	
Ala	Asp	Val	Arg	Glu	Val	Glu	Ser	Gly	Ala	Thr	Met	Gln	Gln	Phe	Ile
			180					185					190		
Asn	Lys	Val	Tyr	Thr	Ala	Ile	Leu	Asn	Leu	Gln	Asn	Asn	Ser	Ala	Lys
		195					200					205			
His	Asn	Glu	Ala	Ala	Gln	Ala	Ser	Gly	Gly	Ala	Val	Gly	Arg	Phe	Thr
	210				215						220				
Thr	Asn	Thr	Lys	Leu	Lys	Asp	Met	Leu	Ile	Val	Thr	Thr	Asp	Glu	Met
225					230					235				240	
Lys	Val	Glu	Ile	Leu	Asn	Ser	Phe	Leu	Ala	Asn	Thr	Phe	His	Ala	Glu
			245					250					255		
Gly	Leu	Asp	Ile	Thr	Ser	Gln	Ile	Ile	Ser	Phe	Glu	Asp	Leu	Gly	Gly
		260						265					270		
Val	Tyr	Lys	Ala	Ala	Glu	Asp	Ile	Thr	Val	Asp	Ala	Thr	Ile	Gln	Gly
		275					280					285			
Val	Met	Ala	Ala	Met	Gly	Asp	Tyr	Gln	Val	Lys	Ala	Gly	Asp	Val	Ile
	290				295					300					
Pro	Ala	Gly	Thr	Val	Phe	Thr	Tyr	Glu	Ile	Pro	Ala	Glu	Ala	Leu	Gly
305					310					315				320	
Asp	Gln	Ala	Asp	Ala	Leu	Val	Glu	Val	Lys	Pro	Asp	Ser	Asp	Glu	Phe
			325						330					335	
Val	Ala	Ile	Phe	Asp	Val	Arg	Ser	Ile	Arg	Tyr	Lys	Arg	Tyr	Thr	Arg
		340					345						350		
Asn	Met	Leu	Lys	Ala	Pro	Phe	Tyr	Asn	Gly	Glu	Phe	Asp	Glu	Val	Thr
		355					360					365			
His	Trp	Ile	His	Tyr	Tyr	Ser	Met	Lys	Ala	Ile	Ser	Pro	Phe	Tyr	Asn
	370					375					380				
Lys	Val	Val	Ile	Lys	Arg	Ala	Asn								
385					390										

<210> 17

<211> 51

<212> PRT

<213> Bacteriophage C1 polypeptide

<400> 17

Met	Leu	Pro	Glu	Glu	His	Thr	Asn	Thr	Ile	His	Asn	Met	Thr	Lys	Asp
1				5					10					15	
Asp	Phe	Gly	Ile	Ser	Lys	Leu	Asp	Lys	Ser	Asn	Glu	Leu	Asn	Glu	Thr
			20					25					30		
Met	Thr	Ile	Gly	Gln	Gly	Lys	Ser	Gln	Asp	Glu	Val	Thr	Thr	Ala	Leu
		35					40					45			
Phe	Asn	Leu													
		50													

<210> 18

<211> 56

<212> PRT

<213> Bacteriophage C1 polypeptide

<400> 18

Met	Thr	Lys	Glu	Glu	Leu	Leu	Ala	Lys	Ile	Ala	Ala	Leu	Glu	Glu	Lys
1				5					10					15	
Thr	Ala	Arg	Leu	Glu	Glu	Leu	Ala	Thr	Ala	Pro	Ala	Pro	Ala	Asp	Glu
			20					25					30		
Pro	Lys	Gln	Gln	Glu	Glu	Gln	Glu	Pro	Glu	Val	Thr	Pro	Ile	Asp	Glu
		35					40					45			
Ile	Glu	Glu	Trp	Leu	Lys	Glu	Asp								
		50				55									

<210> 19

<211> 64

<212> PRT

<213> Bacteriophage C1 polypeptide

<400> 19

Met	Ala	Glu	Asn	Lys	Pro	Leu	Glu	Glu	Gln	Asp	Gly	Lys	Asn	Tyr	Glu
1				5					10					15	
Tyr	His	Ile	Tyr	Ala	Tyr	Val	Asn	Gly	Lys	Trp	Ile	Lys	Val	Tyr	Val
			20					25					30		
Thr	Arg	Asp	Val	Glu	Asp	Arg	Asp	Lys	Val	Met	Leu	Thr	Leu	Lys	Asn
		35					40					45			
Asp	Gly	Asp	Met	Ile	Lys	Asp	Tyr	Phe	Tyr	Glu	Thr	Lys	Glu	Ile	Lys
		50				55					60				

<210> 20

<211> 55

<212> PRT

<213> Bacteriophage C1 polypeptide

<400> 20

Met	Asn	His	Thr	Arg	Thr	Thr	His	Ile	Ser	Val	Thr	Glu	Thr	Ser	Ile
1				5					10					15	
Asp	Thr	Leu	Arg	Asp	Ile	Tyr	Ala	His	Glu	Val	Ala	Thr	Tyr	Gly	Met
			20					25					30		
Glu	Asn	Val	Lys	Val	Val	Ser	Phe	Thr	Met	Asn	Asn	Glu	Gly	Val	Thr
		35					40					45			

Met Val Tyr Asp Ile Ile Lys
50 55

<210> 21
<211> 16687
<212> DNA
<213> Bacteriophage C1 entire genomic sequence

<400> 21
tttttagtata tagcgtagtg atttctccct cccccctcct aatgtaaagt ttttcagaaa 60
acacttttcat aaatatattct gttgacacca cagctgcaac atgatataat taatacataa 120
ataagaaaaga ggtacacaaac atgggttcaca aagtaacaac acgcaaatca ctaactgaca 180
caagcattga cagattgtta agcacatacg cgcagattgt agcgacttac ggctcaccaa 240
atgttcaaat agtccgcttc gttaagaacg gaaatagcgc aacaatgact tacgacataa 300
caatattaat ttaaaaaagt aaacttttcta gttgacaacg acataacggt ttgatataat 360
tagtatataa aatagagata gaggtaacaa caatgacatt tcaaaaagtc cttagatttta 420
aagacgtatc acgtgaagag atgatgaaaa actacagggg attaacagcc cgctatggta 480
tgaataacat catcttagaa gatttgaaat acgacgttga atacaacgaa tactcattca 540
atatactaata caagctataa ggagatattc catgaaaatt agaatagaaa caatttacac 600
tttttcaaca acaatagcaa cactagctct tgggtgtaaac ctattaatgg ataagggaga 660
caacaacaat gttaacactg ataatacttt taataatagc aaccctattg tacaagttga 720
caacaattct agtgaagcca ctactactat tactagtgat actaatgata atcaagtggc 780
tgccgacgat actaatgata ctgaacaact agattatttt caaccatacg aatacctata 840
catgccaaagt acaaacgtat catcaattag agacggatac tacttagtat cagggtggtaa 900
tacattagca gctgttcaaa taacaaatgg ttacacaact gatgaattta gacttaaaaa 960
tatatccgcg gaacaatgga cagtatctca acaacaaatg gaagactttg tttactgggt 1020
acgtgaagtt agtccaagcg gatacaatca aaaaagtcta gaaaataatt ttaaaatttt 1080
tatcaaaaag tagttgacac tgataacaca acatgctata atagatacat aaataagaaa 1140
ggaagtatcc aaaatatgtt ttatacacca attagagagt atagggttaga ttattatgac 1200
ggtgaaaaat accaatcagt catctgcaca gaccatgagt taaatcaaac actatctgaa 1260
ttaatcaata aatcagggtga aagtaatgtc gaaccaataa aggagattag ataatgacag 1320
cttttattga tacaatcaag aaatatcaac ttgaaccaga cgaacaaaaa acggtaacag 1380
tagaaaaaaa aaagtgaaac aaaatataga cgccatcgcc tcattatcaa caagacggta 1440
ttgaacctat tgaatatata atgtcacaca acatgaattt caatatcgga aatgttatca 1500
aatacgtaac aagagcaggc aagaaacagg gtgagcctat agagaaagac ttacaaaaag 1560
caattgatta tttaaagttt gaattagaaa ggggttaaaaa atgaccaaat acctagtaac 1620
tgttatcaac gaccaacacg ttttaagcga acatgaattc acaagtaaga aacacgcttt 1680
aagttttctt aaacgactac aagcagacga aactgtccta tcatcagaaa tagaggaaat 1740
ataatatgaa aacacaagaa tggtagcttag taaatttcgg tttatacgaa accaaaacac 1800
aagaaatgga aacaaattct agatattttg aggataaaca agccgcccta gacttcttct 1860
acactctagc aaacgaggga tactacgact gggcgcatgt atatagcaac ttagaaatgg 1920
aaattatctt ataatgaaac aaacaaatat cgacgcactt ttcggaagag gagaccacca 1980
gttaatgaac aaagaaagta aatacctatc aacattattt atcaatatag aggaattatc 2040
agtacattta tcatcagtaa ctttatattt cgatgaatat gaacagttta aagaaaatgc 2100
tattaagagc aaaaacggta aatgcttgaa actcggtaat acactatact ttaccaataa 2160
taactacgct actaaattat ataatagctt actagcactt ggctttaacg gtgctaacag 2220
cttttcatca ggtgaacaaa catatgttat ttcactaaca ggcggtaatg caacattaac 2280
aactgtcaaa acacattatg gagatgtaaa atatcactat aaacacgaaa aattaccagt 2340
taagaagatt gtcattgatt tctggttatc tgaagactag ggatactcaa cacttaatac 2400
taaattagct tacgcattac ttgatttata taagactatg gataactcaa cacttaatac 2460
tataaaataa tttcaaaaat aagaacaaaa gtattgacaa atataataaa agctgttata 2520
attaatatat ataagttaag taagaaagaa aacttacagt caaactcacg tcaatataaa 2580
aacattagga gaaaaacaaa atggcaatta acttcacaaa catcggattc atcaacttca 2640
acaaagaata caacaaagtt cttaaaaacg gagctatcac agctagcatg tcagcgtcac 2700
aaaaagacgt taaaggtgaa tacgtagacg aatatcacia cgtaactatt cctaaaaaag 2760
tagcagacca aattaaacca cttattaata cagaattatg tgacattcaa ggggttatct 2820

ctcgtaacga	taagtataca	aacatcacca	tcttaggtgc	taaaaaacac	gtcaaagcgg	2880
aagccgtaga	cgtagcagac	gaagatttac	catttctaata	taattaatga	aaggagatga	2940
ggaaaggaca	ataaaaaagtc	tctttcctct	ttttaaatat	atggctaaca	aaagacaacg	3000
taaaaaacaa	ctaaaaacaac	aatatggggt	tggtcataaa	tataccccta	aactaagtca	3060
aacacaacaa	aaacaagctg	attttctaaa	atcaatcggg	caaaaattca	ctaattatca	3120
aacagttaca	attgataaaaa	catattcaaa	aatcaagaa	ttgctagata	cagctaacga	3180
agctcttcat	agactaggta	tcttctttga	tggtagtgaa	aaaatcaagt	tgcagcaggt	3240
gacagatgat	gatttgagat	atatcattaa	taagttacaa	cctcttttgg	aaagtgtgac	3300
aatgagatat	aagaagtttc	tgacaaatac	ataccgctca	aacaatagag	actatcgatt	3360
agactggtta	cttaaatecgg	ccatctctaa	aaaacttaaa	aacgctcaaa	cagttagggg	3420
tctagtagtt	gccatttaata	aaatggatag	agattttaag	gaatacgata	agaaattacg	3480
taaatcaagt	aaacaaggca	acccatttgg	gtttgtcgtt	gtaaaaata	gtgaaatggg	3540
gttaatgtaa	tggcaagaaa	agtaaagaaa	acgataaaaa	caatcttcaa	gaacgaggaa	3600
gaggagttaa	aaacactgct	taatgactat	cgcagaatac	atttaccatc	taaatacaat	3660
caactagaat	tacttgattg	gctatgttca	gacgaaatac	ttcactacat	gtcaataact	3720
tctcgtgggt	acggtaaatc	gtttaattac	attggggcat	tggcatggct	atcatatcat	3780
ttaaactttg	gaactatggt	attggtacgt	cactgggtcat	taatggacaa	aatggctgaa	3840
atgggtatttg	aaattattag	aactgttggg	atgtttgaca	ttgaaaatgt	tgggatacaa	3900
gctaaagctg	attatctaac	aataactatc	gagggctcgag	aagtctttat	tataaccaat	3960
ctaaacaacg	ctagtgactt	gaaacagtca	tcagcggttc	ttcgtacta	cccagttgtt	4020
ttatatgatg	aattcctaac	attaggagag	gattacgtca	caaagtagtt	ggcaaaacta	4080
caaacaatta	tcaagtcctt	tgaccgatg	ggtaaacgac	catacataaa	aaggcctaaa	4140
ataatttatc	taggaaacct	agttaatttt	gacagtccta	ttctaccagc	tctaaacatc	4200
ttctacgcac	tacaaaatca	agaaattaat	actatccaac	aacatggtaa	aacaattctt	4260
gaattacgtc	ggaatgacga	ggtaaacgag	gaaaagacaa	ctggttactt	tgaggatagt	4320
gttgatagtg	atattacagg	tgaatttaac	ttttcaaact	atcggctagc	cgaccaacaa	4380
acataataata	aagcactaac	caacggtaca	ctatataaga	taagactaga	ggacaagctg	4440
tcatacgtta	ttttggaaag	tgacaacgaa	tatatattat	ccatagaaga	aagcaaactt	4500
gatgaaaatt	actgcataca	ccttaaagat	gaaacggcaa	catgtgaata	cctaaaacca	4560
agtttttata	aagatagttt	cataaaacgt	ttccaaaaag	gtcattttta	ctttaaagac	4620
agtttctctc	gtacattcat	tgagggtaac	gaggacttac	aacgcttaaa	cttcttcaaa	4680
cttaacgctg	tagcaagtag	agaccacgaa	gacgcttacg	ccaatattgt	tagggaaagt	4740
tggatttcaa	gacttgctaa	aatctatgaa	aatgatata	atagtttata	gaaagaggtg	4800
tcacaatgaa	agaatttgaa	caatatctaa	agtcattcaa	aggtcaaaag	gttacctctg	4860
ttgacttata	ttgtgatata	gaaaccgcaa	ctattaataa	aaatagcgga	cagaaacacg	4920
ctagtacata	tcactcgttt	acctattcat	tggccgtatc	atacttcaaa	actgggggaag	4980
aattccctag	tgttgctcgtg	tttaatcact	tcaaacagtt	atgttgattt	attgagaaaa	5040
gcaagattag	aaagtctatc	gaatttcgtt	taatatttca	caatggcgct	aaatacgata	5100
atcattttat	ggttagttaa	atacaacgtg	atatagataa	tgtgcgtcta	tttaaccaga	5160
ctattaaaca	agttaaccat	ataacagacc	tagatttatc	aaaaaaacaa	ggtaaacaaa	5220
tgaggaaatga	tgttaaatatg	gtattggaac	gtcgggtacg	ttcatctaata	aaccttgatg	5280
gtgatatgtg	gatatatggc	cgacattatg	aaatggtaga	tagttatcgt	aagactaatg	5340
tgtcaattga	actatgtgga	cgaatgcttc	ttaacaacgg	acttattgac	gaacaatact	5400
taaaaacaga	ttttgagtac	gacaaatacg	atttagatac	agattttaact	tggcacgagg	5460
ttagaaagta	ccgagaattc	atcttcaatg	acttagatga	aaagcagatg	aaatatatcc	5520
ataatgatgt	tattattcta	gccttgacat	gtaaacacta	ctctaaatta	ttttatggat	5580
ttgattttga	gaaacagaca	ttcacacaga	atatcaaaga	ggaatacgca	aactataatg	5640
acatggctaa	attccaactg	ttgaaacaaa	ttggcgataa	catgactggg	aaacacttga	5700
aattaacaga	ctattttatt	caaggtcaaa	atgcttatga	ctactttaaa	aattattata	5760
atggtggcgt	aaacctatat	aacgataaat	atatcggaag	gaaactagtt	agagatgggt	5820
tctctattga	cctgaatagc	tcatatccaa	cagtgatgta	taaggaaaag	ttaccaacct	5880
ttttagtaat	ggtagatagt	aaaccaactg	accttaaaaa	tatcggcagc	actgacgggtg	5940
attatatggg	attttttaac	atgttaatgg	aagatgtaaa	cgaccaaatac	ctatcacgaa	6000
ttaagtctaa	tgttatcaaa	agtgccatag	ttaaatattg	gagagtgaag	gacggctatg	6060
tgtgggttaa	caatgtaatg	attagtttaa	tagaggaaat	aacacatcaa	aaattcaaca	6120
atctacatgt	tcaatcattt	agtgatattt	aatgtcatca	cttcggagct	agggacatta	6180
tagctaaaaa	ttatttcatt	aaaacacaag	gaaagatgag	caaagctctt	aactgtacaa	6240

tggaacaat	tgacccgtta	aacattgaat	taactgataa	ggataaacct	aaagaatatg	6300
acttctccca	tgaaatggta	gaggggttcaa	aggtactact	aaacgggata	tacggtatcc	6360
ctgccttacg	tgcttacttt	gattgttaca	gacgggacga	gaacggtcag	ctgtataacg	6420
tatcaaacgg	ttttgagaat	aaggaacgta	acattgtatt	ttcagcaggt	gtaacagctt	6480
ttgcagtaag	aaacctattg	ctgccactag	gaaaattaac	acaagatgaa	atagatgatt	6540
atctctggta	tgctgatact	gatagtctat	atatggataa	aagagcattg	cctaaactac	6600
ctaaatcaat	gtttcataag	atgaatttag	gaggttggga	tattgaacac	gcaaacatat	6660
ctacattcta	tgccctttaac	cataaaaagt	attgtttata	cgatgatgat	gataatgaaa	6720
tagttgtacg	ttgtgggtgg	atatctaaag	ccttaatcaa	gaaatggata	gctgaaagtc	6780
gcaacaatat	tgattatttt	attaataact	tcttcattga	cgggtgtaaca	atccctgcaa	6840
ccagagctat	aaggaatgaa	tggaatacca	ttacgattta	tgacggcact	agcgaattaa	6900
aaaaaggggg	ggtgtactac	aaaaaatatg	acacgaattt	attacaaaat	attgaaagtg	6960
aattagcaaa	gttaaaagac	gcaatattaa	cagaggaaag	cgaaacaagt	ttagactatt	7020
ccgaaacaat	gtacattgaa	agtaatgtag	gctctttcgg	ggttagcgac	ctatacaaga	7080
ttaaaaagaa	taacactctt	aagcaatcaa	gtatgattgt	agatgagtac	gatgtcttca	7140
aatcatacct	aatctattga	caaataaagg	ccactatgct	ataataagtg	taggaggttt	7200
tttatgatat	atttgttaat	actaaattcc	gctgacttta	ttagcgggat	actcaatggg	7260
attgcattag	gtgacatatc	tagtaagaaa	ctaaaaaaag	gaattattgg	caagtgtctg	7320
caatggattg	ttattgctgt	aacaattaca	atgaaaccag	ttattcatgt	tgacttactt	7380
acatatgtta	tcataacta	ctatataatg	gaagtaattt	ccattcttga	aaacgtcgca	7440
tggtacttac	cagtgcctaa	gaaactgcta	aatgttttag	cacaatttaa	agaaatagaa	7500
aatgaggtaa	aatcaaatga	gcaagattaa	tgtaaacgta	gaaaatgttt	ctgggtgtaca	7560
aggtttccta	ttccataacc	atggaaaaga	aagttacggg	tatcgtgctt	ttattaacgg	7620
agttgaaatt	ggtattaaag	acattgaaac	cgtacaagga	tttcaacaaa	ttataccgtc	7680
tatcaatatt	agtaagtctg	atgtagaggc	tatcagaaaag	gctatgaaaa	agtaatgatt	7740
gaggagtggg	tcaagcaccc	ctccctcaat	tactatataa	gtagttatgg	cagggtgaaa	7800
aactctaaag	gtttaataat	gaaacaacac	atatgcaatg	gttataagcg	aattaaatta	7860
gtaaaggacg	gtataaaaaa	gaattactat	gttcacgcgt	tagttgcaga	aacattcata	7920
cctaaactac	atgttgacta	tggtgtacat	catattgacc	atgataaact	aaacaactgg	7980
gtacataact	tagaatgggtg	tcattatcaa	actaacctat	tatatgaaag	ggagaattta	8040
tttaatgagt	aagaagtata	cacaacaaca	atacgaaaaa	tatttagcac	aaccagcaaa	8100
taacacattt	gggttatcac	ctcaacaggt	tgctgattgg	tttatgggtc	aagctgggtc	8160
taggcctggt	attaactcgt	atggggtaaa	tgctagtaat	ttagtatcaa	cgtacatacc	8220
taaaatgcag	gaatacgggtg	tatcatatac	actattctta	atgtatactg	tctttgaggg	8280
aggcggcgca	ggtaattgga	ttaatcatta	catgtacgat	acgggggtcta	atggattaga	8340
gtgtttggaa	cacgatttac	aatacatata	tggcgtctgg	gaaacttatt	ttccaccagc	8400
tttatctgcg	ccagaatggt	accagctac	ggaagataac	gcaggtgctt	tagatagatt	8460
ttatcaatcg	ctaccaggcc	gaacatgggg	tgatgttatg	atacctagta	caatggctgg	8520
taatgcttgg	gtatgggctt	ataactattg	tgtaacaac	caaggggctg	ccccattagt	8580
ttactttggc	aatccatacg	atagtcaaat	tgatagcttg	cttgcaatgg	gagctgaccc	8640
gtttacaggt	ggttcaatta	caggtgatgg	aaaaaatcct	agtgttggca	ctgggaatgc	8700
taccgtttct	gctagctcgg	aagctaacag	agagaagtta	aagaaagccc	taacagattt	8760
attcaacaac	aacctagaac	atctatcagg	tgaattctac	ggtaaccaag	tgttgaatgc	8820
tatgaaatac	ggcactatcc	tgaaatgtga	tttaacagat	gacggactta	atgccattct	8880
tcaattaata	gctgatgtta	acttacagac	taaccctaac	ccagacaaac	cgaccgttca	8940
atcaccaggt	caaaacgatt	tagggctcggg	gtctgataga	gttgacgcaa	acttagccaa	9000
tgacacggcg	caagtcggta	agtatatgtg	tgacgggtcaa	tgttatgctt	gggttgggtg	9060
gtggtcagct	agggtatgtg	gttattctat	ttcatactca	acaggtgacc	caatgctacc	9120
gttaattggg	gatggtatga	acgctcattc	tatccatctt	ggttgggatt	ggtcaatcgc	9180
aaatactggg	attgttaact	acccagttgg	tactgttggga	cgcaaggaag	atttgagagt	9240
cggcgcgata	tggtgcgcta	cagcattctc	tggcgctccg	ttttatacag	gacaataacg	9300
ccatactggg	atcattgaaa	gctggtcaga	tactaccgtt	acagtcttag	aacaaaacat	9360
tttaggggtca	ccagttatac	gcagcaccta	tgaccttaac	acattcctat	caacactaac	9420
tggttttgata	acattttaaat	aaaaaagaag	agactgtaaa	gtctcttttc	ttatttttata	9480
atgacgttat	taacaactgt	gttattaatc	atgtcacttt	ctttgtgcca	taaccttaca	9540
cctgcttcaa	acaaagctct	taacatatct	atatgccag	tgtctacgtt	aggaagagtc	9600
catattccct	tgaattgaac	ccaattacaa	attgacatag	atgtaatgtc	tgaaagtttt	9660

gttgaatagt	cgttacactc	atatccgaac	atgttgtaat	acttcttaac	attgttttaac	9720
tcgtcttg	atatacgacc	caatctcaag	tgtacaccga	atgtgtcttg	tttaaataaaa	9780
ggagcatatc	caacatgccc	ctccgtaatg	gcatttggtg	aagcgtccat	ttgttttaaac	9840
tgggcttttt	ggtctctgta	gtgttcatat	tcattgttaa	aacctgatag	tgctgactta	9900
atagacagtc	cacctgacag	agaaatagca	ttgaacagtc	tatctttaac	actggcgtca	9960
ttgtcaagta	cggatttgat	acgtgatgac	atgtgacgtg	aattagataa	ctcacgacta	10020
taggctgaat	tggcttttcc	taactcacca	ctgtcaacag	agaaacctat	agtatcaaag	10080
ttatattattg	tgagggcatt	gtcaatgtat	tgaccaacgt	tgttacctct	agcgttatag	10140
tttttaacat	atacctttat	ttcgttcttc	gctcccatag	ttacaaaact	atcaaattca	10200
agattagttt	caattaaaga	aaggtcgatt	ggtaaacgat	taccagcgta	atctgttagc	10260
tcggctgtta	ctatattagg	ccttagtaaa	tgtttatcat	tgattgggtt	taaacctagc	10320
gtaaacataa	gtgattgata	atctaaacta	atagcattaa	aatctttttg	atgtgataca	10380
ccctgcttac	ctaattttacg	aacagacaaa	tcaccaccgt	taactgggtc	gtggctggtt	10440
aaactttctt	gtttaataaaa	gccacttgga	ataattgtta	cgttttttat	tgattgttgt	10500
atccaagggg	agcctgtgag	atagtcatt	acctctttta	gactttcata	gtcattaaac	10560
caatacagg	gtaaatgggt	gtaaatacca	tcattgtgtg	aaccactaga	agatggaaat	10620
ttaggctttt	ctgccgtacc	aaaagattta	cgtaagttag	ctcctattgt	tagtatgtac	10680
tcaagttgtg	tgaacaactc	tgatttgata	gcgtgtactc	tcatagtgct	tgtagctaaa	10740
acgtcattgt	tagaacgaat	ttgttctaaa	ttctgttcat	attcagtttg	agtataatgt	10800
tgacgtataa	cattaacgtt	attgagtgtg	tttaatacat	ttccttgagt	atatgtcata	10860
acaacgtctg	gtactagaga	cagttcacat	accttgatcat	taagttgttg	aatgtcagtt	10920
acaaataagt	attcaactct	gtttgattga	atgtattgta	cttgacagta	gttaacgccc	10980
attaactgct	caaagcatga	acggtcactt	actaagtcta	ttgtaaccct	tagcaccctt	11040
ttcatattcc	tatagttaaa	tgttgatgta	aactcatgta	catcaaactt	actattgaaa	11100
taggcgtccc	gttcctcatt	tgaattgaaa	tgcaaagtat	tttgcagtgt	gttaaaccggt	11160
gtattataga	ataattttat	ttttgataag	gtcattcttt	ttgtcctcct	gcttctatta	11220
taccataaaa	acactagcta	ggctagtgtt	attgtttatt	tttctagttt	ttcttttgata	11280
aactcatcaa	tttgtttctg	ttcaactttc	ttgtcgtaca	ttggctctct	tagtaattca	11340
ttgatttggt	cttgtgttag	tgccattgtt	tatctccttt	ctagctgtaa	aagctcttcta	11400
cagttaccca	ttgattaaat	ggtttatgtt	tataaccgtc	tgcttggtaa	gctggcatgt	11460
attctgtacc	cgttacaggg	tctaaccatg	tttcaataac	atatgggtga	ccagttgcag	11520
gtgctctaaa	gttatctaga	gactcagtat	ctaaaccact	agttccta	ccttgggcca	11580
ctaggtacat	ttcttcttta	tcgtcattat	cgtataacgt	gaacacaacg	ggataaccatt	11640
ttttaacttg	tgcgttggtta	tcaaattggg	ggaagtcatt	cattgtgata	gcattgtttg	11700
atagaacatg	tttcaacccta	tcagttacac	cctctgcgta	aatgtcta	atgaaataat	11760
acatgtctgc	aacttgttca	ggccaccag	tgccctctaaa	tgtcatatgc	cagatgtcta	11820
acaaaaggaa	ttcaaaacgt	ttagtaacgc	cccgcacttg	gaatgtatgg	gattgatata	11880
gtaggttcat	tccgccgtta	gggtcaatct	gcgtaccagt	gctagcattt	ccaactgggt	11940
taaacctaat	agcttttgac	ccctcacgac	taccgaatgt	tgctaagctg	ttcatcattt	12000
ctgtatatgt	tgaattttgt	ttcacaccta	gaatatctgc	gtctaacaat	tcaatctttt	12060
gtgttagtgg	gtcaatatct	ggtatgtcaa	gagcaattaa	tcgtttttcc	atgttatcaa	12120
tttgaagtgt	tagacctgcg	tcagcttctc	cgaattcctg	cgataaattc	tcaatcatag	12180
ctcggatttg	ttccattggt	acgtctgaac	cctctggcgt	tagaatttca	tcaattagtt	12240
gctcaatttc	agcaatttta	gatgtgtagt	caacgacgtg	taaccctgca	gttgtgattt	12300
ttaaaccggt	atctgattgt	ggtgctacct	taacatctac	ctgaatgcc	ttatagatat	12360
ttgacttggc	tgttgatgtt	tcagcaccct	ttaaattacc	aagaagattt	ttattctcgg	12420
ccgcttgggc	agcaacttcg	tcaatttggt	gaatgatttc	aaggctcgga	ttttttaaat	12480
cttgtagctc	tttatcgtga	ccatcaagtc	taccgtcttg	ttcgatatct	ttttcactgt	12540
tagcgttaat	agcgtctgct	actgccttac	taaattgtaa	ttctttccaa	tgttcatggg	12600
cgtgatgtga	catgtggctg	tgatgttggt	caaattggatt	gatataaaat	ttcatataat	12660
tagtaccctt	catagaatag	ttggctgaat	aatttaatat	ctagctcatc	aaaaatcttc	12720
tgcttaaatg	tctcgtatct	ttctaaagct	ttagtgttaa	attgtgtgtt	ggttgaattt	12780
gaattattgt	cactacttcc	ctgactacta	ctgataccct	ttgaatgtga	tacgttaaca	12840
ctttcgttat	agctcttatc	aaggttatct	gcatagctta	ggttagctgt	ttctaggctg	12900
gtatcggtta	catcatcagg	gtttgttgag	tgagcgttag	ctcctctggt	ttcaccggtta	12960
ctttcgtttg	tgctgttatc	tcgacttcta	ttctcattag	atgaatgtcc	ctcactctta	13020
gacatgcttt	cacctaataa	taattctggt	gatttttaagt	acaacatatt	tagcacagct	13080

tcttttgttt	ttagtattcc	ttttagtttc	gctctaaaga	tgtatagact	gtcccaatgt	13140
ggctctctgt	taaagaagta	gttaacgaat	tcctctctaa	agtccttcgt	taccttgctg	13200
ccagtgaaga	taagttcatt	aacaaccttt	tgtacatctt	catcatacat	cattatcttt	13260
gtttcaatth	gtgctttgtc	ctcaaact	acaattctat	tttcagggct	gcggaacgg	13320
gaataaccgt	tctttaccac	ttctttataa	attaactcga	ataatctcat	tgtgctacct	13380
cgcttacaat	ttgaagcttc	tcaataactg	ataattcagc	aaccatatta	tccctgtatt	13440
cagcatgaat	attaaggccg	tatttattat	taataagggt	taaggcttcg	ttgcgaattc	13500
caagataaat	gttttcgttt	gctttcttaa	aggctgtatt	ggattgggct	tcaatttctg	13560
atacgccact	ttctttatca	actcctagag	tatttagtcc	tagcattgca	ttcaattcag	13620
aaattttatt	ctgttggtca	cgtttcaatt	ctggtaagaa	tgaaacagcc	gaggcattat	13680
tgaatgtag	tatatgttcc	tctgggtcga	atttaggcgt	tgttgctgta	taaggtagac	13740
cgtaaaaaag	attattggcc	atgacttgac	cgcttttgct	gccacctca	ttacgtataa	13800
aggtattaac	cttagcttga	atggaaatac	tataacttga	attggctatt	tcagacattt	13860
ccataacata	atgtgtaata	atgttataat	cgcacaagaa	actagctctt	ttgttacgta	13920
atacaacaaa	attaccatca	ctgtatcttg	ttagctcttt	atactttcct	ttgggtagta	13980
tgttattgtg	aatgaatgtg	atgtctttgc	cttgtagagg	ctctttaatt	ggttgtaagt	14040
aatttgtatt	tacagaacaa	tatcctagta	cgtaactctt	accagtttta	gtttcaccca	14100
tggccacccc	gtaccagca	cgtaaataac	tttcgattag	taaactatct	aaatcatagt	14160
tttcatatga	aattagtagt	ggtaggaatt	ctacatatct	actataaata	atattaaagt	14220
agttttgttt	atgtaacttt	accctttcag	ctatatcatc	tgtaaaagta	gacattttgt	14280
aattcatttc	actaggctta	attcctgatg	tgatttgcat	gtataccctt	ttctatataa	14340
aaacagagga	cttgccgccc	cgtaatttag	ttagcacgct	taattactac	cttattgtag	14400
aaaggactaa	tagctttcat	tgagtagtag	tgaatccaat	gtgttacttc	gtcaaaactca	14460
ccgttataga	atgggtgctt	caacatgtta	cgtgtataac	gtttgtaacg	aattgaacgt	14520
acatcgaaaa	ttgttacaaa	ttcatcactg	tcaggtttaa	cttcgactag	agcgtcagct	14580
tggctgcccc	gagcttctgc	gggaatttgc	taagtgaata	ctgttcctgc	tgggataaca	14640
tcacctgctt	taacttggta	gtctcccatg	gcagccatca	caccttgaat	agttgcgctg	14700
actgtaatgt	cctcggctgc	tttatataca	ccgcctaagt	cttcaaaaaga	gataatttgt	14760
gatgtaatat	ccaatccctc	tgctggaat	gtgttagcaa	ggaagctgtt	taggatttca	14820
actttcattt	cgtcagttgt	aacaattaac	atatccttta	gttttgtgtt	tgttgtaaaa	14880
cgccgactg	cacctcctga	agcttgtgca	gcttcgttat	gcttagcaga	gttggtttgt	14940
aagttaagga	tactgtgata	aactttgttg	atgaattgtt	gcattgtagc	acctgattca	15000
aactcacgta	cgctgcaata	gtgacttgtg	tagtccataa	taatagcctt	tagctcttgt	15060
tcctctgaaa	gtttaatatc	agcgattttc	tttttgtaga	cttgtactgc	aaactttgtt	15120
gcgtctccta	gagtagcaaa	ttgttgacgt	tggatattgt	cattaagagt	gaatttaagt	15180
tttttaagaa	tacctgcacc	gtacaactta	gaagcaattt	ttggatagtt	gcgttctagc	15240
ataagttgtg	ctgattttga	taagtcaagt	tcaactggga	cggtgtcaag	gataacgtat	15300
tcttctgaat	attgtccgat	aaagtcaatt	tcttttgcga	gccaatctaa	acggttacct	15360
gctgctgttt	caacaattag	ggtctcgttc	aatttaggga	aaagatatgt	attagtatat	15420
gtctcgaagt	ctgtaccaac	tgcatcccaa	ttagtaccga	atgtccaaga	tttaccgtta	15480
tctgcgttaa	aatcggttaag	tgaagcgaca	atagcgccag	ctacgtttgt	agtttcatct	15540
gccataatat	ataattctcc	tattttctat	tttttctatt	tattataagt	taaacaaagc	15600
tgttggttact	tcgtcttgtg	atttaccttg	gccaatcgtc	atagtttctg	taagttcatt	15660
tgacttatcg	agctttgaaa	taccgaagtc	atctttggtc	atgttgtgga	ttgtgtttgt	15720
gtgttcttct	ggtagcatgt	tatttagtct	cctttaacca	ttcttcaatt	tcgtcaattg	15780
gtgtaacttc	tggctcttgt	tcttcttgtc	gttttggttc	atcagcagga	gcaggagcgg	15840
tagctagtct	ttcaagacgt	gctgtctttt	cttcaagagc	tgcaatctta	gctagtattt	15900
cttctttctg	cattaaatag	tctcctttca	aaataaaaata	tcggtatttt	tacttggtta	15960
tccgataaac	aaagttaggt	ctaggggttc	tctaattatg	tgcttatagt	ctcgtatgac	16020
ctcaattcta	attaataact	cttccctatt	tccttactac	tctttaatta	tatcaaaacta	16080
tttagatat	gtcaagcttt	tttatttaat	tttcttttgt	tcgtagaaat	agtctttaat	16140
catatcacgc	tcatttttaa	gagtttagcat	aactttgtct	ctatcctcta	catcacaggt	16200
aacgtatact	ttaatccatt	taccattaac	atatgcgtag	atgtggtact	catagttttt	16260
accgtcttgt	tcctctagt	gtttgttttc	agccatttgt	attctccttt	ccttatttgt	16320
atatatagta	taacaaattg	tttcgtgatt	gtcaactgtt	ttatttgaag	tttttaaat	16380
tattttataa	tgtcgtaaac	cattgttacg	ccctcattgt	tcatagtga	gctgactacc	16440
ttaacatttt	ccataaccata	agttgcaacc	tcattgtcat	atatatcgcg	tagcgtgtca	16500

```

atgcttggtt  cggttactga  tatgtgtgtt  gttcgtgtgt  ggttcatgtt  gtgtacctct  16560
ttcttattta  tgtattaatt  atatcatgtt  gcagctgtgg  tgtcaacaga  aatatttatg  16620
aaagtgtttt  ctgaaaacat  ttacattagg  aggggggagg  gagaaatcac  tacgctatat  16680
actaaaa                                16687

```

<210> 22

<211> 219

<212> DNA

<213> Bacteriophage C1 light chain of PlyC (PlyC B)
(formerly known as gene for alpha subunit)

<400> 22

```

atgagcaaga  ttaatgtaaa  cgtagaaaat  gtttctggtg  tacaagggtt  cctattccat  60
accgatggaa  aagaaagtta  cggttatcgt  gcttttatta  acggagttga  aattgggtatt  120
aaagacattg  aaaccgtaca  aggatttcaa  caaattatac  cgtctatcaa  tattagtaag  180
tctgatgtag  aggctatcag  aaaggctatg  aaaaagtaa                                219

```

<210> 23

<211> 1419

<212> DNA

<213> Bacteriophage C1 heavy chain of PlyC (PlyC A)
(formerly known as gene for beta subunit)

<400> 23

```

atgaaaggga  gaatttatTT  aatgagtaag  aagtatacac  aacaacaata  cgaaaaatat  60
ttagcacaac  cagcaaataa  cacatttggg  ttatcacctc  aacagggtgc  tgattgggtt  120
atgggtcaag  ctggtgctag  gcctgttatt  aactcgtatg  gggtaaattg  tagtaattta  180
gtatcaacgt  acatacctaa  aatgcaggaa  tacgggtgat  catatacact  attcttaatg  240
tatactgtct  ttgagggagg  cggcgcagg  aattggatta  atcattacat  gtacgatacg  300
gggtctaatt  gattagagtg  tttggaacac  gattttacaat  acatacatgg  cgtctgggaa  360
acttattttc  caccagcttt  atctgcgcca  gaatgttacc  cagctacgga  agataacgca  420
ggtgctttag  atagatttta  tcaatcgcta  ccaggccgaa  catgggggtg  tgttatgata  480
cctagtacaa  tggctggtaa  tgcttgggta  tgggcttata  actattgtgt  taacaaccaa  540
ggggctgccc  cattagttta  ctttggcaat  ccatacgata  gtcaaattga  tagcttgctt  600
gcaatgggag  ctgaccctgt  tacagggtgt  tcaattacag  gtgatggaaa  aaatcctagt  660
gttggcactg  ggaatgctac  cgtttctgct  agctcggaag  ctaacagaga  gaagttaaag  720
aaagccctaa  cagattttat  caacaacaac  ctagaacatc  tatcagggtg  attctacggt  780
aaccaagtgt  tgaatgctat  gaaatacggc  actatcctga  aatgtgattt  aacagatgac  840
ggacttaatt  ccattcttca  attaatagct  gatgttaact  tacagactaa  ccctaacca  900
gacaaaccga  ccgttcaatc  accagggtcaa  aacgatttag  ggtcgggggtc  tgatagagtt  960
gcagcaaact  tagccaatgc  acaggcgcaa  gtcggtaagt  atattgggtg  cgggtcaatgt  1020
tatgcttggg  ttggttggtg  gtcagctagg  gtatgtgggt  attctatttc  atactcaaca  1080
ggtgacccaa  tgctaccgtt  aattgggtgat  ggtatgaacg  ctattcttat  ccatcttggt  1140
tggtgattgt  caatcgcaaa  tactgggtatt  gttaactacc  cagttgggtac  tggtggacgc  1200
aaggaagatt  tgagagtctg  cgcatatagg  tgcgtacag  cattctcttg  cgctccgttt  1260
tatacaggac  aatacggcca  tactgggtatc  attgaaagct  ggtcagatac  taccgttaca  1320
gtcttagaac  aaaacatttt  agggtcacca  gttatacgca  gcacctatga  ccttaacaca  1380
ttcctatcaa  cactaactgg  ttgataaca  tttaaataa                                1419

```

<210> 24

<211> 318

<212> DNA

<213> Bacteriophage C1 lysin intergenic locus(lil)

<400> 24

```

atgattgagg  agtgggtcaa  gcaccctctc  ctcaattact  atataagtag  ttatggcagg  60
gtgaaaaact  ctaaagggtt  aataatgaaa  caacacatat  gcaatggtta  taagcgaatt  120

```

aaattagtaa	aggacggtat	aaaaaagaat	tactatgttc	atcgcttagt	tgcagaaaca	180
ttcataccta	aactacatgt	tgactatggt	gtacatcata	ttgaccatga	taaactaaac	240
aactgggtac	ataaacttaga	atgggtgcat	tatcaaacta	acctattata	tgaaagggag	300
aatttattta	atgagtaa					318

<210> 25

<211> 2213

<212> DNA

<213> Bacteriophage C1 PlyC operon

<400> 25

gaagtaattt	ccattcttga	aaacgtcgca	tggtacttac	cagtgccaaa	gaaactgcta	60
aatgttttag	cacaatttaa	agaaatagaa	aatgaggtaa	aatcaaatga	gcaagattaa	120
tgtaaacgta	gaaaatgttt	ctgggtgtaca	aggtttccta	ttccataccg	atggaaaaga	180
aagttacggt	tatcgtgctt	ttattaacgg	agttgaaatt	ggtattaaag	acattgaaac	240
cgtacaagga	tttcaacaaa	ttataccgtc	tatcaatatt	agtaagtctg	atgtagaggc	300
tatcagaaag	gctatgaaaa	agtaatgatt	gaggagtggg	tcaagcacc	ctccctcaat	360
tactatataa	gtagttatgg	cagggtgaaa	aactctaaag	gtttaataat	gaaacaacac	420
atatgcaatg	gttataagcg	aattaaatta	gtaaaggacg	gtataaaaa	gaattactat	480
gttcatcgct	tagttgcaga	aacattcata	cctaaactac	atgttgacta	tgttgtacat	540
catattgacc	atgataaact	aaacaactgg	gtacataact	tagaatgggt	tcattatcaa	600
actaacctat	tatatgaaag	ggagaattta	tttaatgagt	aagaagtata	cacaacaaca	660
atacgaaaa	tatttagcac	aaccagcaaa	taacacattt	gggttatcac	ctcaacaggt	720
tgctgattgg	tttatgggtc	aagctgggtc	taggcctgtt	attaactcgt	atgggggtaa	780
tgctagtaat	ttagtatcaa	cgtacatacc	taaaatgcag	gaatacgggt	tatcatatac	840
actattctta	atgtatactg	tctttgaggg	aggcgccgca	ggtaattgga	ttaatcatta	900
catgtacgat	acgggggtcta	atggattaga	gtgtttggaa	cacgatttac	aatacataca	960
tggcgctctg	gaaacttatt	ttccaccagc	tttatctgcg	ccagaatgtt	acccagctac	1020
ggaagataac	gcaggtgctt	tagatagatt	ttatcaatcg	ctaccaggcc	gaacatgggg	1080
tgatgttatg	atacctagta	caatggctgg	taatgcttgg	gtatgggctt	ataactattg	1140
tgtaacaac	caaggggctg	ccccattagt	ttactttggc	aatccatacg	atagtcaaat	1200
tgatagcttg	cttgcaatgg	gagctgacc	gtttacaggt	ggttcaatta	caggtgatgg	1260
aaaaaatcct	agtgttggca	ctgggaatgc	taccgtttct	gctagctcgg	aagctaacag	1320
agagaagtta	aagaaagccc	taacagattt	attcaacaac	aacctagaac	atctatcagg	1380
tgaattctac	ggtaaccaag	tgttgaatgc	tatgaaatac	ggcactatcc	tgaaatgtga	1440
tttaacagat	gacggactta	atgccattct	tcaattaata	gctgatgtta	acttacagac	1500
taaccctaac	ccagacaaac	cgaccgttca	atcaccaggt	caaaacgatt	tagggtcggg	1560
gtctgataga	gttgacgcaa	acttagccaa	tgcacaggcg	caagtcggta	agtatattgg	1620
tgacgggtcaa	tgttatgctt	gggttggttg	gtggtcagct	agggtatgtg	gttattctat	1680
ttcatactca	acaggtgacc	caatgctacc	gttaattggg	gatggtatga	acgctcattc	1740
tatccatctt	ggttgggatt	ggtcaatcgc	aaatactggg	attgttaact	acccagttgg	1800
tactgttgga	cgcaagggaag	atgtgagagt	cggcgcgata	tggtgcgcta	cagcattctc	1860
tggcgctccg	ttttatacag	gacaatacgg	ccatactggg	atcattgaaa	gctggtcaga	1920
tactaccggt	acagtcttag	aacaaaacat	tttaggggtca	ccagttatac	gcagcaccta	1980
tgaccttaac	acatttcctat	caacactaac	tggtttgata	acattttaat	aaaaaagaag	2040
agactgtaaa	gtctcttttc	ttattttata	atgacgttat	taacaactgt	gttattaatc	2100
atgtcacttt	ctttgtgcca	taaccttaca	cctgcttcaa	acaaagctct	taacatattc	2160
atatgcccg	tgtctacgtt	aggaagagtc	catattccct	tgaattgaac	cca	2213

<210> 26

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 26	
gtacccgggg aagtaatttc cattcttgaa	30
<210> 27	
<211> 30	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> primer	
<400> 27	
cccaagcttt tactttttca tagcctttct	30
<210> 28	
<211> 38	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> primer	
<400> 28	
gtacccgggga ggaggaattc atgattgagg agtggggtc	38
<210> 29	
<211> 36	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> primer	
<400> 29	
gggaagcttt tactcattaa ataaattctc cctttc	36
<210> 30	
<211> 30	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> primer	
<400> 30	
gtacccggga aagggaagaat ttatttaatg	30
<210> 31	
<211> 30	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> primer	
<400> 31	
cccaagcttt gggttcaatt caagggaata	30